

2128 #2



OIPE

RAW SEQUENCE LISTING

DATE: 03/12/2002

PATENT APPLICATION: US/10/025,730

TIME: 10:49:40

Input Set : N:\Crf3\RULE60\10025730.raw

Output Set: N:\CRF3\03122002\J025730.raw

ENTERED

1 <110> APPLICANT: Tang, Y. Tom
 2 Guegler, Karl J.
 3 Corley, Neil C.
 4 Gorgone, Gina A.
 5 <120> TITLE OF INVENTION: CALCIUM BINDING PROTEIN
 6 <130> FILE REFERENCE: PF-0635 US
 7 <140> CURRENT APPLICATION NUMBER: 10/025,730
 8 <141> CURRENT FILING DATE: 2001-12-18
 10 <150> PRIOR APPLICATION NUMBER: US/09/190,965
 11 <151> PRIOR FILING DATE: 1998-11-13
 13 <160> NUMBER OF SEQ ID NOS: 5
 14 <170> SOFTWARE: PERL Program
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 337
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Homo sapiens
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 21 <223> OTHER INFORMATION: 3734805
 22 <400> SEQUENCE: 1
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 24 1 5 10 15
 25 Glu Ile Val Lys Ile Leu Lys Asp Asn Leu Ala Ile Leu Glu Lys
 26 20 25 30
 27 Gln Asp Lys Lys Thr Asp Lys Ala Ser Glu Glu Val Ser Lys Ser
 28 35 40 45
 29 Leu Gln Ala Met Lys Glu Ile Leu Cys Gly Thr Asn Glu Lys Glu
 30 50 55 60
 31 Pro Pro Thr Glu Ala Val Ala Gln Leu Ala Gln Glu Leu Tyr Ser
 32 65 70 75
 33 Ser Gly Leu Leu Val Thr Leu Ile Ala Asp Leu Gln Leu Ile Asp
 34 80 85 90
 35 Phe Glu Gly Lys Lys Asp Val Thr Gln Ile Phe Asn Asn Ile Leu
 36 95 100 105
 37 Arg Arg Gln Ile Gly Thr Arg Ser Pro Thr Val Glu Tyr Ile Ser
 38 110 115 120
 39 Ala His Pro His Ile Leu Phe Met Leu Lys Gly Tyr Glu Ala
 40 125 130 135
 41 Pro Gln Ile Ala Leu Arg Cys Gly Ile Met Leu Arg Glu Cys Ile
 42 140 145 150
 43 Arg His Glu Pro Leu Ala Lys Ile Ile Leu Phe Ser Asn Gln Phe
 44 155 160 165
 45 Arg Asp Phe Phe Lys Tyr Val Glu Leu Ser Thr Phe Asp Ile Ala
 46 170 175 180

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47 Ser Asp Ala Phe Ala Thr Phe Lys Asp Leu Leu Thr Arg His Lys
48                               185                               190                               195
49 Val Leu Val Ala Asp Phe Leu Glu Gln Asn Tyr Asp Thr Ile Phe
50                               200                               205                               210
51 Glu Asp Tyr Glu Lys Leu Leu Gln Ser Glu Asn Tyr Val Thr Lys
52                               215                               220                               225
53 Arg Gln Ser Leu Lys Leu Leu Gly Glu Leu Ile Leu Asp Arg His
54                               230                               235                               240
55 Asn Phe Ala Ile Met Thr Lys Tyr Ile Ser Lys Pro Glu Asn Leu
56                               245                               250                               255
57 Lys Leu Met Met Asn Leu Leu Arg Asp Lys Ser Pro Asn Ile Gln
58                               260                               265                               270
59 Phe Glu Ala Phe His Val Phe Lys Val Phe Val Ala Ser Pro His
60                               275                               280                               285
61 Lys Thr Gln Pro Ile Val Glu Ile Leu Leu Lys Asn Gln Pro Lys
62                               290                               295                               300
63 Leu Ile Glu Phe Leu Ser Ser Phe Gln Lys Glu Arg Thr Asp Asp
64                               305                               310                               315
65 Glu Gln Phe Ala Asp Glu Lys Asn Tyr Leu Ile Lys Gln Ile Arg
66                               320                               325                               330
67 Asp Leu Lys Lys Thr Ala Pro
68                               335

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70 <210> SEQ ID NO: 2

71 <211> LENGTH: 1344

72 <212> TYPE: DNA

73 <213> ORGANISM: Homo sapiens

W--> 74 <220> FEATURE: -

75 <223> OTHER INFORMATION: 3734805

76 <400> SEQUENCE: 2

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77 cagaaacaga actgcctgtg acagattaag agacaagcaa ggcttggaat ctgagagcaa 60
78 gcaaagagag tggaaaattta cagctgcctt atcattccat attggaagaa gagatttcta 120
79 cacatgaaaa aaatgccttt gtttagtaaa tcacacaaaa atccagcaga aattgtgaaa 180
80 atcctgaaag acaatttggc cattttggaa aagcaagaca aaaagacaga caaggcttca 240
81 gaagaagtgt ctaaattcact gcaagcaatg aaagaaattc tgtgtggtac aaacgagaaa 300
82 gaacccccga cagaagcagt ggctcagcta gcacaagaac tctacagcag tggcctgctg 360
83 gtgacactga tagctgacct gcagctgata gactttgagg gaaaaaaaga tgtgaccag 420
84 atatttaaca acatcttgag aagacagata ggcaactcga gtcctactgt ggagtatt 480
85 agtgctcatc ctcatatcct gtttatgctc ctcaaaggat atgaagcccc acagattgcc 540
86 ttacgttggtg ggattatgct gagagaatgt attcgacatg aaccacttgc caaaatcatc 600
87 ctcttttcta atcaattcag agatttcttt aagtacgtgg agttgtcaac atttgatatt 660
88 gcttcagatg cctttgctac tttcaaggat ttactaacca gacataaagt gttggtagca 720
89 gacttccttag aacaaaatta cgacactatt tttgaagact atgagaaatt gcttcagtct 780
90 gagaattatg ttactaagag acagtcttta aagctgctag gggagctgat cctggaccgt 840
91 cacaactttg ccatcatgac aaagtatatc agcaagccgg agaacctgaa actcatgatg 900
92 aacctccttc gggataaaaag tccaacatc cagtttgaag cctttcatgt ttttaagggtg 960
93 tttgtggcca gtcctcaca aacacagcct attgtggaga tcctgttaaa aaatcagccc 1020
94 aaactcattg agtttctgag cagcttccaa aaagaaagga cggatgatga gcagttcgct 1080
95 gacgagaaga actacttgat taaacagatc cgagacttga agaaaacggc cccttgaaga 1140
96 gctccccggc ccctgtcaca gtcagtcgtc tcatttgtcc agtttgtaca gtgtgtcatt 1200

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Input Set : N:\Crf3\RULE60\10025730.raw

Output Set: N:\CRF3\03122002\J025730.raw

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97      tcagaaagtc atcattcttg ggaagacttt ggaggtgcct attttttctg ctgtaattgt 1260
98      tctgggtaga tggagtataa acatttgaat ggaaaaaaat taacctagaa taatatattc 1320
99      atttttagtca aaaaaaaaaa aaaa                                     1344
101 <210> SEQ ID NO: 3
102 <211> LENGTH: 341
103 <212> TYPE: PRT
104 <213> ORGANISM: Mus sp.
W--> 105 <220> FEATURE: -
106 <223> OTHER INFORMATION: g262934
107 <400> SEQUENCE: 3
108      Met Pro Phe Pro Phe Gly Lys Ser His Lys Ser Pro Ala Asp Ile
109      1                    5                    10                    15
110      Val Lys Asn Leu Lys Glu Ser Met Ala Val Leu Glu Lys Gln Asp
111      20                    25                    30
112      Ile Ser Asp Lys Lys Ala Glu Lys Ala Thr Glu Glu Val Ser Lys
113      35                    40                    45
114      Asn Leu Val Ala Met Lys Glu Ile Leu Tyr Gly Thr Asn Glu Lys
115      50                    55                    60
116      Glu Pro Gln Thr Glu Ala Val Ala Gln Leu Ala Gln Glu Leu Tyr
117      65                    70                    75
118      Asn Ser Gly Leu Leu Gly Thr Leu Val Ala Asp Leu Gln Leu Ile
119      80                    85                    90
120      Asp Phe Glu Gly Lys Lys Asp Val Ala Gln Ile Phe Asn Asn Ile
121      95                    100                   105
122      Leu Arg Arg Gln Ile Gly Thr Arg Thr Pro Thr Val Glu Tyr Ile
123      110                   115                   120
124      Cys Thr Gln Gln Asn Ile Leu Phe Met Leu Leu Lys Gly Tyr Glu
125      125                   130                   135
126      Ser Pro Glu Ile Ala Leu Asn Cys Gly Ile Met Leu Arg Glu Cys
127      140                   145                   150
128      Ile Arg His Glu Pro Leu Ala Lys Ile Ile Leu Trp Ser Glu Gln
129      155                   160                   165
130      Phe Tyr Asp Phe Phe Arg Tyr Val Glu Met Ser Thr Phe Asp Ile
131      170                   175                   180
132      Ala Ser Asp Ala Phe Ala Thr Phe Lys Asp Leu Leu Thr Arg His
133      185                   190                   195
134      Lys Leu Leu Ser Ala Glu Phe Leu Glu Gln His Tyr Asp Arg Phe
135      200                   205                   210
136      Phe Ser Glu Tyr Glu Lys Leu Leu His Ser Glu Asn Tyr Val Thr
137      215                   220                   225
138      Lys Arg Gln Ser Leu Lys Leu Leu Gly Glu Leu Leu Leu Asp Arg
139      230                   235                   240
140      His Asn Phe Thr Ile Met Thr Lys Tyr Ile Ser Lys Pro Glu Asn
141      245                   250                   255
142      Leu Lys Leu Met Met Asn Leu Leu Arg Asp Lys Ser Arg Asn Ile
143      260                   265                   270
144      Gln Phe Glu Ala Phe His Val Phe Lys Val Phe Val Ala Asn Pro
145      275                   280                   285
146      Asn Lys Thr Gln Pro Ile Leu Asp Ile Leu Leu Lys Asn Gln Thr

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DATE: 03/12/2002

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TIME: 10:49:40

Input Set : N:\Crf3\RULE60\10025730.raw

Output Set: N:\CRF3\03122002\J025730.raw

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147          290          295          300
148      Lys Leu Ile Glu Phe Leu Ser Lys Phe Gln Asn Asp Arg Thr Glu
149          305          310          315
150      Asp Glu Gln Phe Asn Asp Glu Lys Thr Tyr Leu Val Lys Gln Ile
151          320          325          330
152      Arg Asn Leu Lys Arg Ala Ala Gln Gln Glu Ala
153          335          340
155 <210> SEQ ID NO: 4
156 <211> LENGTH: 339
157 <212> TYPE: PRT
158 <213> ORGANISM: Drosophila melanogaster
W--> 159 <220> FEATURE: -
160 <223> OTHER INFORMATION: g1794137
161 <400> SEQUENCE: 4
162      Met Pro Leu Phe Gly Lys Ser Gln Lys Ser Pro Val Glu Leu Val
163          1          5          10          15
164      Lys Ser Leu Lys Glu Ala Ile Asn Ala Leu Glu Ala Gly Asp Arg
165          20          25          30
166      Lys Val Glu Lys Ala Gln Glu Asp Val Ser Lys Asn Leu Val Ser
167          35          40          45
168      Ile Lys Asn Met Leu His Gly Ser Ser Asp Ala Glu Pro Pro Ala
169          50          55          60
170      Asp Tyr Val Val Ala Gln Leu Ser Gln Glu Leu Tyr Asn Ser Asn
171          65          70          75
172      Leu Leu Leu Leu Leu Ile Gln Asn Leu His Arg Ile Asp Phe Glu
173          80          85          90
174      Gly Lys Lys His Val Ala Leu Ile Phe Asn Asn Leu Leu Arg Arg
175          95          100          105
176      Gln Ile Gly Thr Arg Ser Pro Thr Val Glu Tyr Ile Cys Thr Lys
177          110          115          120
178      Pro Glu Ile Leu Phe Thr Leu Met Ala Gly Tyr Glu Asp Ala His
179          125          130          135
180      Pro Glu Ile Ala Leu Asn Ser Gly Thr Met Leu Arg Glu Cys Ala
181          140          145          150
182      Arg Tyr Glu Ala Leu Ala Lys Ile Met Leu His Ser Asp Glu Phe
183          155          160          165
184      Phe Lys Phe Phe Arg Tyr Val Glu Val Ser Thr Phe Asp Ile Ala
185          170          175          180
186      Ser Asp Ala Phe Ser Thr Phe Lys Glu Leu Leu Thr Arg His Lys
187          185          190          195
188      Leu Leu Cys Ala Glu Phe Leu Asp Ala Asn Tyr Asp Lys Phe Phe
189          200          205          210
190      Ser Gln His Tyr Gln Arg Leu Leu Asn Ser Glu Asn Tyr Val Thr
191          215          220          225
192      Arg Arg Gln Ser Leu Lys Leu Leu Gly Glu Leu Leu Leu Asp Arg
193          230          235          240
194      His Asn Phe Thr Val Met Thr Arg Tyr Ile Ser Glu Pro Glu Asn
195          245          250          255
196      Leu Lys Leu Met Met Asn Met Leu Lys Glu Lys Ser Arg Asn Ile

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TIME: 10:49:40

Input Set : N:\Crf3\RULE60\10025730.raw

Output Set: N:\CRF3\03122002\J025730.raw

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197          260          265          270
198    Gln Phe Glu Ala Phe His Val Phe Lys Val Phe Val Ala Asn Pro
199          275          280          285
200    Asn Lys Pro Lys Pro Ile Leu Asp Ile Leu Leu Arg Asn Gln Thr
201          290          295          300
202    Lys Leu Val Asp Phe Leu Thr Asn Phe His Thr Asp Arg Ser Glu
203          305          310          315
204    Asp Glu Gln Phe Asn Asp Glu Lys Ala Tyr Leu Ile Lys Gln Ile
205          320          325          330
206    Lys Glu Leu Lys Pro Leu Pro Glu Ala
207          335
209 <210> SEQ ID NO: 5
210 <211> LENGTH: 377
211 <212> TYPE: PRT
212 <213> ORGANISM: Caenorhabditis elegans
W--> 213 <220> FEATURE: -
214 <223> OTHER INFORMATION: g1255838
215 <400> SEQUENCE: 5
216    Met Pro Leu Leu Phe Gly Lys Ser His Lys Ser Pro Ala Asp Val
217      1          5          10          15
218    Val Lys Thr Leu Arg Glu Val Leu Thr Ile Leu Asp Lys Leu Pro
219          20          25          30
220    Pro Pro Lys Leu Asp Lys Asp Gly Asn Ile Gln Ser Asp Lys Lys
221          35          40          45
222    Tyr Asp Lys Ala Leu Asp Glu Val Ser Lys Asn Val Ala Met Ile
223          50          55          60
224    Lys Ser Phe Ile Tyr Gly Asn Asp Ser Ala Glu Pro Ser Ser Glu
225          65          70          75
226    His Val Val Gln Val Ala Gln Leu Ala Gln Glu Val Tyr Asn Ala
227          80          85          90
228    Asn Ile Leu Pro Met Leu Ile Lys Met Leu Pro Lys Phe Glu Phe
229          95          100          105
230    Glu Cys Lys Lys Asp Val Gly Gln Ile Phe Asn Asn Leu Leu Arg
231          110          115          120
232    Arg Gln Ile Gly Thr Arg Ser Pro Thr Val Glu Tyr Leu Gly Ala
233          125          130          135
234    Arg Pro Glu Ile Leu Ile Gln Leu Val Gln Gly Tyr Ser Val Pro
235          140          145          150
236    Asp Ile Ala Leu Thr Cys Gly Leu Met Leu Arg Glu Ser Ile Arg
237          155          160          165
238    His Asp His Leu Ala Lys Ile Ile Leu Tyr Ser Asp Val Phe Tyr
239          170          175          180
240    Thr Phe Phe Leu Tyr Val Gln Ser Glu Val Phe Asp Ile Ser Ser
241          185          190          195
242    Asp Ala Phe Ser Thr Phe Lys Glu Leu Thr Thr Arg His Lys Ala
243          200          205          210
244    Ile Ile Ala Glu Phe Leu Asp Ser Asn Tyr Asp Thr Phe Phe Ala
245          215          220          225
246    Gln Tyr Gln Asn Leu Leu Asn Ser Lys Asn Tyr Val Thr Arg Arg

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/025,730

DATE: 03/12/2002

TIME: 10:49:41

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Output Set: N:\CRF3\03122002\J025730.raw

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L:159 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:213 M:256 W: Invalid Numeric Header Field, <220> has non-blank data